

SEQUENCE LISTING

<110> GRAY, Kevin A.
ABOUSHADI, Nahla
GARRETT, James B.

<120> AMYLASES, NUCLEIC ACIDS ENCODING THEM AND METHODS
FOR MAKING AND USING THEM

<130> 564462003900

<140> US 10/532,944

<141> 2003-10-15

<150> PCT/US03/33150

<151> 2003-10-15

<150> US 60/423,626

<151> 2002-10-31

<160> 24

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Gly Ile Ile Asp Arg Leu Glu Tyr Val Ala Ala Leu Gly Val Asp Ala
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Ile Trp Val Ser Pro Phe Phe Thr Ser Pro Met Ala Asp Phe Gly Tyr
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Asp Phe Asp Arg Leu Leu Ala Lys Ala His Ala Leu Gly Leu Lys Val
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Arg Glu Ser Arg Gln Asp Arg Thr Asn Pro Lys Ala Asp Trp Tyr Val
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Trp Ala Asp Pro Arg Glu Asp Gly Thr Pro Pro Asn Asn Trp Met Ser
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Ile Phe Gly Gly Val Ala Trp Gln Trp Glu Pro Arg Arg Glu Gln Tyr
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Asp Pro Tyr Gly Ile Thr Phe Trp Pro Asn Phe Lys Gly Arg Asp Gly
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			485						490						495
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Arg Pro Gly Thr Ala Trp Trp Ala Pro Ala Phe Glu Ser Asn Arg Glu
165 170 175
Glu Tyr Leu Tyr Asn Gln Thr Pro Ile Asp Gly Val Ala Ile Ala Met
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Thr Pro Phe Thr Met Arg Phe Glu Asp Gly Thr His Leu Ser Ile His
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Glu Ala Ala Leu Val Asp Tyr Ser Gly Met Asn Val Thr Arg Val Gln
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 Gly Glu Glu Leu Gly Leu Phe Glu Val Ala Asp Ile Pro Trp Asp Arg
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<210> 8
 <211> 781
 <212> PRT
 <213> Bacteria

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Arg Pro Ser Arg Phe Asp Val Asp His Asp Gly Trp Ala Thr Val Gln
          35          40          45
Tyr Asp Ala Gly Val Met Val Gly Val Ala Ala Leu Asp Asp Thr Val
          50          55          60
Leu Arg Val Ala Tyr Cys Arg Ser Pro Gly Glu Trp Pro Thr Ser Thr
          65          70          75          80
Pro Ala Ile Val Glu Gln Met Ser Gln Arg His Ser Trp Arg Leu Val
          85          90          95
Gln Glu Glu Arg Arg Val Gln Leu Glu Cys Val Ala Gly Trp Gln Ile
          100          105          110
Gln Ile Asn Arg Asp Asp Gly Thr Trp Ser Ile Arg His Leu Gly Phe
          115          120          125
Gly Thr Ala Val Glu Ala Ile Thr Trp Tyr Lys Arg Lys Lys Gly Gly
          130          135          140
Ala Leu Thr Phe Ala Ser Leu Asp Asn Ala Arg Phe Tyr Gly Leu Gly
          145          150          155          160
Glu Lys Pro Gly Pro Leu Asp Lys Arg His Glu Ala Tyr Thr Met Trp
          165          170          175
Asn Ser Asp Val Tyr Ala Pro His Val Pro Glu Met Glu Ala Leu Tyr
          180          185          190
Leu Ser Ile Pro Phe Phe Leu Arg Leu Gln Asp Gln Thr Ala Val Gly
          195          200          205
Ile Phe Val Asp Asn Pro Gly Arg Ser Arg Phe Asp Phe Arg Ser Arg
          210          215          220
Tyr Pro Asp Val Glu Ile Ser Thr Glu Arg Gly Gly Leu Asp Val Tyr
          225          230          235          240
Phe Ile Phe Gly Ala Ser Leu Lys Asp Val Ile Arg Arg Tyr Thr Lys
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Gln	Thr	Phe	Val	Glu	Arg	Asp	Ile	Pro	Val	Asp	Ala	Leu	Tyr	Leu	Asp		
	290					295					300						
Ile	His	Tyr	Met	Asp	Gly	Tyr	Arg	Val	Phe	Thr	Phe	Asp	Glu	Arg	Arg		
305					310					315					320		
Phe	Pro	Asp	Pro	Ala	Arg	Met	Cys	Asp	Glu	Leu	Arg	Lys	Leu	Gly	Val		
			325						330					335			
Arg	Val	Val	Pro	Ile	Val	Asp	Pro	Gly	Val	Lys	Gln	Asp	Pro	Glu	Tyr		
		340						345					350				
Pro	Val	Tyr	Met	Asp	Gly	Leu	Ala	His	Asn	His	Phe	Cys	Gln	Thr	Ala		
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	370					375					380						
Pro	Asp	Phe	Ala	Ser	Glu	Glu	Val	Arg	Ala	Trp	Trp	Gly	Lys	Trp	His		
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Arg	Val	Tyr	Thr	Gln	Met	Gly	Ile	Glu	Gly	Ile	Trp	Asn	Asp	Met	Asn		
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His	Arg	Gly	Asp	Gly	Arg	Leu	Tyr	Thr	His	Gly	Glu	Val	His	Asn	Leu		
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Tyr	Gly	Phe	Trp	Met	Ala	Glu	Ala	Thr	Tyr	Arg	Gly	Leu	Lys	Ala	Gln		
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Leu	Ala	Gly	Lys	Arg	Pro	Phe	Val	Leu	Thr	Arg	Ala	Gly	Tyr	Ser	Gly		
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Ile	Gln	Arg	Tyr	Ala	Ala	Val	Trp	Thr	Gly	Asp	Asn	Arg	Ser	Phe	Trp		
			485						490					495			
Glu	His	Met	Ala	Met	Ala	Ile	Pro	Met	Val	Leu	Asn	Met	Gly	Met	Ser		
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Gly	Ile	Pro	Leu	Gly	Gly	Pro	Asp	Val	Gly	Gly	Phe	Ala	His	His	Ala		
	515					520						525					
Ser	Gly	Glu	Leu	Leu	Ala	Arg	Trp	Thr	Gln	Met	Gly	Ala	Phe	Phe	Pro		
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Phe	Phe	Arg	Asn	His	Ser	Ala	Met	Gly	Thr	His	Arg	Gln	Glu	Pro	Trp		
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Ala	Phe	Gly	Pro	Thr	Phe	Glu	Ala	Val	Ile	Arg	Arg	Ala	Ile	Arg	Leu		
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Arg	Tyr	Arg	Phe	Leu	Pro	Tyr	Leu	Tyr	Thr	Leu	Ala	Arg	Glu	Ala	His		
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Glu	Thr	Gly	Leu	Pro	Met	Met	Arg	Pro	Leu	Val	Leu	Glu	Tyr	Pro	Asp		
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Asp	Pro	Asn	Thr	His	His	Val	Asp	Asp	Gln	Phe	Leu	Val	Gly	Ser	Asp		
	610				615						620						
Leu	Leu	Val	Ala	Pro	Ile	Leu	Lys	Pro	Gly	Met	Ala	His	Arg	Met	Val		
	625				630					635					640		
Tyr	Leu	Pro	Asp	Gly	Glu	Trp	Ile	Asp	Tyr	Glu	Thr	Arg	Glu	Arg	Tyr		
			645						650					655			
Gln	Gly	Arg	Gln	Tyr	Ile	Leu	Thr	Tyr	Ala	Pro	Leu	Asp	Arg	Ile	Pro		
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Leu	Tyr	Val	Arg	Ala	Gly	Ser	Ala	Ile	Pro	Val	Asn	Leu	Leu	Glu	Arg		
	675					680						685					
Ser	Gly	Glu	Thr	Gln	Leu	Gly	Trp	Glu	Ile	Phe	Val	Asp	Ala	Asn	Gly		
	690				695					700							
Arg	Ala	Ser	Gly	Arg	Cys	Tyr	Glu	Asp	Asp	Gly	Glu	Thr	Phe	Ser	Tyr		
	705				710					715					720		
Glu	Asp	Gly	Ala	Tyr	Cys	Asp	Arg	Val	Leu	Gln	Ala	Leu	Ala	Thr	Ser		
			725						730					735			
Glu	Gly	Thr	Leu	Ile	Glu	Cys	His	Leu	Val	Gln	Gly	Ser	Gly	Asp	Gly		
		740						745					750				
Gly	Ser	Leu	Glu	Ser	Val	Val	Arg	Val	Phe	Thr	Pro	Asp	Asp	Val	Arg		
	755						760						765				

~~PC~~ ~~Glu~~ ~~Ala~~ ~~Arg~~ ~~Ala~~ ~~Gln~~ ~~Gly~~ ~~Ala~~ ~~Ser~~ ~~Phe~~ ~~Ser~~ ~~Leu~~ ~~His~~ ~~Val~~
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<210> 9

<211> 1611

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 9

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gatcttggcg	tggacgcggt	ctggctgtca	ccgttcttca	aaagcccgat	gaaggacatg	180
ggctatgacg	tcagcgacta	ttgcgatgtc	gatccgggtct	tcggcaccct	cgccgatttt	240
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ctgtcgggtgt	tcgggtggctc	ggcatggggc	tgggacgcgc	gcagaaaaca	gtattacctg	480
cacaatttcc	tgaccagcca	gccggacctg	aactaccaca	acccgaaggt	gcaggactgg	540
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cggtttcttg	atctggccga	accggttctg	ggctttgtgc	gcggcggaag	ggagggtgcg	1440
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<210> 10

<211> 536

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 10

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			20					25					30		
Thr	Ala	Arg	Leu	Glu	Tyr	Leu	Ala	Asp	Leu	Gly	Val	Asp	Ala	Val	Trp
		35				40					45				
Leu	Ser	Pro	Phe	Phe	Lys	Ser	Pro	Met	Lys	Asp	Met	Gly	Tyr	Asp	Val
	50				55					60					
Ser	Asp	Tyr	Cys	Asp	Val	Asp	Pro	Val	Phe	Gly	Thr	Leu	Ala	Asp	Phe
65				70					75					80	
Asp	Ala	Leu	Leu	Ala	Arg	Ala	His	Glu	Leu	Gly	Leu	Lys	Val	Ile	Ile
				85				90						95	
Asp	Gln	Val	Leu	Ser	His	Ser	Ser	Asp	Leu	His	Pro	Ala	Phe	Val	Thr
		100						105					110		
Ser	Arg	Ser	Asp	Arg	Val	Asn	Pro	Lys	Ala	Asp	Trp	Tyr	Val	Trp	Ala

Asp	Pro	Lys	Pro	Asp	Gly	Ser	Pro	Pro	Asn	Asn	Trp	Leu	Ser	Val	Phe
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Gly	Gly	Ser	Ala	Trp	Ala	Trp	Asp	Ala	Arg	Arg	Lys	Gln	Tyr	Tyr	Leu
145					150					155					160
His	Asn	Phe	Leu	Thr	Ser	Gln	Pro	Asp	Leu	Asn	Tyr	His	Asn	Pro	Lys
			165						170					175	
Val	Gln	Asp	Trp	Ala	Leu	Asp	Asn	Met	Arg	Phe	Trp	Leu	Asp	Arg	Gly
			180					185					190		
Val	Asp	Gly	Phe	Arg	Phe	Asp	Thr	Val	Asn	Tyr	Phe	Phe	His	Asp	Pro
		195					200					205			
Leu	Leu	Arg	Ser	Asn	Pro	Ala	Asp	His	Arg	Asn	Lys	Pro	Glu	Ala	Asp
		210				215					220				
Gly	Asn	Pro	Tyr	Gly	Met	Gln	Tyr	His	Leu	His	Asp	Lys	Asn	Gln	Pro
225					230					235					240
Glu	Asn	Leu	Ile	Trp	Met	Glu	Arg	Ile	Arg	Val	Leu	Leu	Asp	Gln	Tyr
			245						250					255	
Gly	Ala	Ala	Ser	Val	Gly	Glu	Met	Gly	Glu	Ser	His	His	Ala	Ile	Arg
			260					265					270		
Met	Met	Gly	Asp	Tyr	Thr	Ala	Pro	Gly	Arg	Leu	His	Gln	Cys	Tyr	Ser
		275					280					285			
Phe	Glu	Phe	Met	Gly	Tyr	Glu	Tyr	Thr	Ala	Asn	Leu	Phe	Arg	Asp	Arg
		290				295					300				
Ile	Glu	Ser	Phe	Phe	Lys	Gly	Ala	Pro	Lys	Gly	Trp	Pro	Met	Trp	Ala
305					310					315					320
Phe	Ser	Asn	His	Asp	Val	Val	Arg	His	Val	Ser	Arg	Trp	Ala	Lys	His
			325						330					335	
Gly	Leu	Thr	Pro	Glu	Ala	Val	Ala	Lys	Gln	Thr	Gly	Ala	Leu	Leu	Leu
			340					345					350		
Ser	Leu	Glu	Gly	Ser	Ile	Cys	Leu	Trp	Glu	Gly	Glu	Glu	Leu	Gly	Gln
		355					360					365			
Thr	Asp	Thr	Glu	Leu	Ala	Leu	Asp	Glu	Leu	Thr	Asp	Pro	Gln	Gly	Ile
		370				375					380				
Val	Phe	Trp	Pro	Glu	Pro	Ile	Gly	Arg	Asp	Asn	Thr	Arg	Thr	Pro	Met
385					390					395					400
Val	Trp	Asp	Ala	Ser	Pro	His	Gly	Gly	Phe	Ser	Thr	Val	Thr	Pro	Trp
			405						410					415	
Leu	Pro	Val	Lys	Pro	Glu	Gln	Ala	Ala	Arg	His	Val	Ala	Gly	Gln	Thr
			420					425				430			
Gly	Asp	Ala	Ala	Ser	Val	Leu	Glu	Ser	Tyr	Arg	Ala	Met	Leu	Ala	Phe
		435					440				445				
Arg	Arg	Ala	Glu	Pro	Ala	Leu	Arg	Thr	Gly	Arg	Thr	Arg	Phe	Leu	Asp
		450				455					460				
Leu	Ala	Glu	Pro	Val	Leu	Gly	Phe	Val	Arg	Gly	Glu	Gly	Glu	Gly	Ala
465					470					475					480
Ile	Leu	Cys	Leu	Phe	Asn	Leu	Ser	Pro	Val	Ala	Arg	Gly	Val	Ala	Val
			485						490					495	
Glu	Gly	Val	Gly	Pro	Pro	Ile	Gly	Pro	Gly	Gln	Gln	Ala	Ile	Leu	Ser
			500					505					510		
Gly	Gly	Arg	Leu	Gly	Leu	Gly	Pro	Asn	Gly	Ala	Ala	Phe	Leu	Arg	Val
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<210> 11

<211> 1719

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 11

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gattgcggct acgatatcag cgattaccgc aacgttgctc cggaatacgg cagcgtggac 240
gatttcaaaa ccttcctgag cgaatcgac aaacgcggta tccgcgtcat tctcgacctc 300
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aatcccaaat ccgattggta tgtgtgggtc gatacgccgc ccaacaattg gcagtcctgc 420
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gcggtgcgct tctggctcga tctcggcgtg gacggcttcc gcctggacgc catcggcacg 600
atctacgaag acccaaatct cagcccgcat aatgtcccga tgaatttggc tgagctgcgt 660
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<211> 572

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 12

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20          25          30
Gly Ile Ile Gly Lys Leu Asp Tyr Leu Gln Asn Leu Gly Ile Asp Ala
35          40          45
Leu Trp Leu Ser Pro His Phe Pro Ser Pro Asn Trp Asp Cys Gly Tyr
50          55          60
Asp Ile Ser Asp Tyr Arg Asn Val Ala Pro Glu Tyr Gly Thr Leu Asp
65          70          75          80
Asp Phe Lys Thr Phe Leu Ser Glu Ser His Lys Arg Gly Ile Arg Val
85          90          95
Ile Leu Asp Leu Val Leu Asn His Thr Ser Asp Glu His Pro Trp Phe
100          105          110
Ile Glu Ser Lys Ser Ser Arg Asp Asn Pro Lys Ser Asp Trp Tyr Val
115          120          125
Trp Val Asp Thr Pro Pro Asn Asn Trp Gln Ser Cys Phe Asp Gly Asp
130          135          140
Ala Trp Thr Tyr Val Pro Glu Arg Gly Gln Tyr Tyr Tyr His Tyr Phe
145          150          155          160
Met Lys Gln Gln Pro Asp Leu Asn Trp His Asn Pro Gln Val Lys Gln
165          170          175
Ala Met Trp Glu Ala Val Arg Phe Trp Leu Asp Leu Gly Val Asp Gly
180          185          190
Phe Arg Leu Asp Ala Ile Gly Thr Ile Tyr Glu Asp Pro Asn Leu Thr
195          200          205

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PC Pro His Asp Val Pro Met Asn Ile Ala Glu Leu Arg His Phe Thr Asp
 210 215 220
 Val Ala Lys Thr Pro Glu Ile Lys Leu Lys Glu Lys Tyr Trp His
 225 230 235 240
 Asp Met Phe Lys His Gln Trp Gly Gln Pro Gly Val His Asp Leu Met
 245 250 255
 Lys Glu Leu Arg Ala Ile Leu Asp Glu Tyr Asp Gly Asp Arg Met Leu
 260 265 270
 Val Gly Glu Asp Asp Asn Ile Asp Tyr Met Gly Asn Gly Asp Asp Glu
 275 280 285
 Leu Gln Leu Val Phe Asn Phe Pro Leu Met Arg Ala Asp Arg Leu Thr
 290 295 300
 Pro Asp His Ile Arg Arg Asn Gln Lys Glu Arg Leu Thr Arg Leu Asn
 305 310 315 320
 Ala Leu Pro Val Lys Gly Trp Ala Cys Asn Thr Leu Gly Asn His Asp
 325 330 335
 Ser Ser Arg Val Tyr Thr Lys Phe Gly Asp Arg Ile His Gly Ala Asp
 340 345 350
 His Ala Arg Leu Asn Leu Ala Leu Leu Leu Thr Leu His Gly Thr Pro
 355 360 365
 Phe Leu Tyr Asn Gly Glu Glu Ile Gly Met Thr Asp His Ile Ile Thr
 370 375 380
 Asp Pro Thr Lys Leu Arg Asp Thr Met Ala Thr Trp Tyr Tyr Asn Ser
 385 390 395 400
 Leu Val Asn Glu Met Lys Val Glu Pro Ala Glu Ala Ala Leu Arg Ala
 405 410 415
 Gly Gln Met Thr Arg Asp Lys Asn Arg Thr Pro Met Gln Trp Asp Asn
 420 425 430
 Lys Pro Asn Ala Gly Phe Cys Pro Asp Lys Ala Glu Pro Trp Leu Pro
 435 440 445
 Val Asn Pro Asn Tyr Arg Ala Gly Ile Asn Val Arg Glu Gln Thr Ser
 450 455 460
 Asn Pro Asn Ser Leu Leu Asn Tyr Tyr Lys Arg Leu Ile His Leu Arg
 465 470 475 480
 Arg Glu Thr Pro Ala Leu Ile Ala Gly Asp Tyr Val Pro Leu His Gln
 485 490 495
 Thr Ser Lys Asp His Leu Ala Phe Leu Arg Lys Thr Asp Ser Gln Thr
 500 505 510
 Ile Leu Val Val Leu Asn Tyr Ser Pro Asn Lys Leu Glu Leu Asp Phe
 515 520 525
 Ser Arg Thr Val Glu Met Lys Gly Arg Pro Leu Ile Ala Ile Phe Ser
 530 535 540
 Ser Ala Asp Asp Arg Pro Gln Ala Ala Gln Ser Pro Lys Lys Val Ser
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 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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 cggatgaggg aaatatgtga gagacacggc tattacaggg gaataaata tagtgcgagtgg 360
 aacatgggtca gcgactacca caccatatgg ggctactacc agttcaaact agcactaagc 420
 attgccaagg acgtcgagga ttacgctccc gatgcatggc ttatcaacgt cgctaatacca 480

~~gtgttccgaat~~ ~~tgcacacact~~ ~~gatccagagg~~ ~~taacggaaga~~ taaagatgat agggctgtgc 540
catggatacc acggcatata taatgtcatg aaagaactag gcctaccacg agaagaaaca 600
gagttcgagg tactaggatt caaccacgtc atatggctta caaagttcaa gtaccagga 660
gaagacgctt acccgttact agacaagtgg atcgaggaga aagcagagaa gtactgggag 720
cattggagac aaacacaggt aaacccgttc gacatcgact tgtcgccggc agcgatagac 780
atgtacaaga gatacgggtc cctcccggtg ggagacactg tgcgtggagg gacgtggatg 840
taccactggg atctcaagac gaagcagaaa tggatatggc cgacaggagg accagactcc 900
gagataggct ggatgatgta tatagccttc ctaagcatgc agctccaaag actatacgaa 960
gcactaacgg atcagaagca cccgtagca gcacatgtac cgccggagtg gagcgggtgaa 1020
tccatagtcc caataatcga tagcctcgcc aacaatagga ggggagaata cgttatcaac 1080
acgttgaatc tgggcagcat acccgggata cgggataatg tggctgtcga gatgccggcc 1140
cagatagatg gtaaaggagt gcaccgctac atattcgagc cactcccaa gaagataaga 1200
gacctggctc tactgcctag gatgaccgt atggagatgg cattgacagc cttcctcgag 1260
ggaggccgtg aagtactaga ggactggcta cacatggatc cacgtaccaa gagcactaga 1320
caggtaacggg agacaatcga tgatctcctt aacatgcccc gtaacgagga gatgaagaag 1380
catttcagct aa 1392

<210> 14
<211> 463
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 14
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Ala Gly Ser Ala Val Trp Ser Ser Arg Ile Ile Val Asp Leu Ile Leu
20 25 30
Ala Lys Ser Leu His Gly Ala Lys Ile Tyr Leu Met Asp Ile Asn Lys
35 40 45
Glu Arg Leu Asp Leu Ile Thr Gly Phe Ala Lys Arg Tyr Ala Ala Glu
50 55 60
Met His Ala Asp Leu Glu Phe Ile Pro Thr Met Asp Arg Val Glu Ala
65 70 75 80
Ile Arg Asp Ala Asp Phe Val Val Asn Ser Ala Met Tyr Gly Gly His
85 90 95
Met Tyr Tyr Glu Arg Met Arg Glu Ile Cys Glu Arg His Gly Tyr Tyr
100 105 110
Arg Gly Ile Asn Ser Val Glu Trp Asn Met Val Ser Asp Tyr His Thr
115 120 125
Ile Trp Gly Tyr Tyr Gln Phe Lys Leu Ala Leu Ser Ile Ala Lys Asp
130 135 140
Val Glu Asp Tyr Ala Pro Asp Ala Trp Leu Ile Asn Val Ala Asn Pro
145 150 155 160
Val Phe Glu Leu Thr Thr Leu Ile Gln Arg His Val Lys Ile Lys Met
165 170 175
Ile Gly Leu Cys His Gly Tyr His Gly Ile Tyr Asn Val Met Lys Glu
180 185 190
Leu Gly Leu Pro Arg Glu Glu Thr Glu Phe Glu Val Leu Gly Phe Asn
195 200 205
His Val Ile Trp Leu Thr Lys Phe Lys Tyr Gln Gly Glu Asp Ala Tyr
210 215 220
Pro Leu Leu Asp Lys Trp Ile Glu Glu Lys Ala Glu Lys Tyr Trp Glu
225 230 235 240
His Trp Arg Gln Thr Gln Val Asn Pro Phe Asp Ile Asp Leu Ser Pro
245 250 255
Ala Ala Ile Asp Met Tyr Lys Arg Tyr Gly Leu Leu Pro Val Gly Asp
260 265 270
Thr Val Arg Gly Gly Thr Trp Met Tyr His Trp Asp Leu Lys Thr Lys
275 280 285
Gln Lys Trp Tyr Gly Pro Thr Gly Gly Pro Asp Ser Glu Ile Gly Trp
290 295 300

PC Met Met Tyr Ile Ala Phe Leu Ser Met Gln Leu Gln Arg Leu Tyr Glu
 305 310 315 320
 Ala Leu Thr Asp Gln Lys His Pro Leu Ala Ala His Val Pro Pro Glu
 325 330 335
 Trp Ser Gly Glu Ser Ile Val Pro Ile Ile Asp Ser Leu Ala Asn Asn
 340 345 350
 Arg Arg Gly Glu Tyr Val Ile Asn Thr Leu Asn Leu Gly Ser Ile Pro
 355 360 365
 Gly Ile Pro Asp Asn Val Ala Val Glu Met Pro Ala Gln Ile Asp Gly
 370 375 380
 Lys Gly Val His Arg Tyr Ile Phe Glu Pro Leu Pro Lys Lys Ile Arg
 385 390 395 400
 Asp Leu Val Leu Leu Pro Arg Met Thr Arg Met Glu Met Ala Leu Thr
 405 410 415
 Ala Phe Leu Glu Gly Gly Arg Glu Val Leu Glu Asp Trp Leu His Met
 420 425 430
 Asp Pro Arg Thr Lys Ser Thr Arg Gln Val Arg Glu Thr Ile Asp Asp
 435 440 445
 Leu Leu Asn Met Pro Gly Asn Glu Glu Met Lys Lys His Phe Ser
 450 455 460

<210> 15
 <211> 1632
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 15
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 gcgtcgatct accagattta cccgcgcagt tttgcggaca gcaacgggtga tggcggtggc 120
 gaccttgccg ggattacttc gcatctggag catatcgca gcctgggtgt ggaggcgatc 180
 tggatcagcc cgtttttcac cagcccgatg gccgattatg gctatgacgt ggccgattat 240
 tgcgatgtcg atccgatctt cgggaactttg gcggacttcg atgcgctggt cgagaaggcc 300
 catgggctgg gcctgaaggt caccatcgac atggtctttg cccataccag cgacaggcat 360
 ccgtgggtcg aacaatcgcg ttcggcgcgc gagaatgacc gcgccgactg gtacgtctgg 420
 gccgatccca agccggacgg cagccgcgcc aacaactggc agtcggtgtt tggcggcccg 480
 gcctggacct gggacgcgcg gcgcgggcag tactacatgc accagtccct gaaggagcag 540
 ccgcaattga acgcgcacaa tcctgcggtg caggatgcgc tgctcgatgc cttgcgcttc 600
 tggctggagc ggggggtgga cgggttcggg ctcgatgcgc tgaaccactc gatgttcgat 660
 ccggcgctga ccgacaatct gcccgcgccc gaggatggca agatccgcac gcggcctttc 720
 gattttcagt tgaaaatcaa cagccagaac catcccgtg tgacgctgtt catcgagcgg 780
 atcgccgatg tttgcggcca gcatggcgcg gtcttcaccg tggccgaagt gggcggcgat 840
 ggcgcggttc cgctgatgaa ggcgtacacg gcgggcgagc atcggtgtc ctcggcctac 900
 agctttgatt tcctttatgc gccggccttg acgggcgagc tgggtggcaa tgctctggcc 960
 cagtggacgg gcaagccggg ggccgatggg ctgagcgaag gctggcccag ctgggcgttt 1020
 gagaaccatg atgcgcccg ccatatctcg cgctgggtgg gcgaggagca tcgcgccgcc 1080
 tttgcccgga tgagccttgt gctgctggcc tcgctgcgcg gtaacatgtt catgtatcag 1140
 gggcaggaac tggcgctgga gcaggatgag atcccgtttc atctgctgaa agaccccgag 1200
 gcgatcgcca actggccgct gacgttgagc cgcgacgggg tgcgcacgcc gatgccatgg 1260
 gacagccagg ccttccatgc cggcttcacg agtggcgagc cctggttgcc cttgtcgccg 1320
 ggggaatatcg ccaaggcggt ggatgtgcag gaggccgatc cgcagagcca gctgcactgg 1380

 gtgcggcggg ttctggccct gcgcgcgcgg cacaaggccc tgcgtctggg cgcgatggag 1440
 catgtgcata tgcagggcga tgtgctcagt ttcaccgcgc atgcgcgcgg cgaaagggtg 1500
 gagtgcgtgt tcaacctttc cgccaaaacc gtcgccaca aggcgcacaa gggtagacg 1560
 ctgctcaccg tcaatggcgc aaccggggcg gtgttgacgc catatggcgc tctctggacg 1620
 aaactcgcat aa 1632

<210> 16
 <211> 543
 <212> PRT

<220>

<223> Obtained from an environmental sample

<400> 16

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Trp	Trp	His	Gly	Ala	Ser	Ile	Tyr	Gln	Ile	Tyr	Pro	Arg	Ser	Phe	Ala
		20						25					30		
Asp	Ser	Asn	Gly	Asp	Gly	Val	Gly	Asp	Leu	Ala	Gly	Ile	Thr	Ser	His
		35					40					45			
Leu	Glu	His	Ile	Ala	Ser	Leu	Gly	Val	Glu	Ala	Ile	Trp	Ile	Ser	Pro
	50					55					60				
Phe	Phe	Thr	Ser	Pro	Met	Ala	Asp	Tyr	Gly	Tyr	Asp	Val	Ala	Asp	Tyr
65				70					75					80	
Cys	Asp	Val	Asp	Pro	Ile	Phe	Gly	Thr	Leu	Ala	Asp	Phe	Asp	Ala	Leu
				85					90					95	
Val	Glu	Lys	Ala	His	Gly	Leu	Gly	Leu	Lys	Val	Thr	Ile	Asp	Met	Val
			100					105					110		
Phe	Ala	His	Thr	Ser	Asp	Arg	His	Pro	Trp	Phe	Glu	Gln	Ser	Arg	Ser
		115				120						125			
Ala	Arg	Glu	Asn	Asp	Arg	Ala	Asp	Trp	Tyr	Val	Trp	Ala	Asp	Pro	Lys
	130					135					140				
Pro	Asp	Gly	Thr	Pro	Pro	Asn	Asn	Trp	Gln	Ser	Val	Phe	Gly	Gly	Pro
145				150					155					160	
Ala	Trp	Thr	Trp	Asp	Ala	Arg	Arg	Gly	Gln	Tyr	Tyr	Met	His	Gln	Phe
				165				170						175	
Leu	Lys	Glu	Gln	Pro	Gln	Leu	Asn	Ala	His	Asn	Pro	Ala	Val	Gln	Asp
			180					185					190		
Ala	Leu	Leu	Asp	Ala	Leu	Arg	Phe	Trp	Leu	Glu	Arg	Gly	Val	Asp	Gly
		195					200					205			
Phe	Arg	Leu	Asp	Ala	Leu	Asn	His	Ser	Met	Phe	Asp	Pro	Ala	Leu	Thr
	210					215					220				
Asp	Asn	Leu	Pro	Ala	Pro	Glu	Asp	Gly	Lys	Ile	Arg	Thr	Arg	Pro	Phe
225				230					235					240	
Asp	Phe	Gln	Leu	Lys	Ile	Asn	Ser	Gln	Asn	His	Pro	Ala	Val	Thr	Leu
				245					250					255	
Phe	Ile	Glu	Arg	Ile	Ala	Asp	Val	Cys	Gly	Gln	His	Gly	Ala	Val	Phe
			260					265					270		
Thr	Val	Ala	Glu	Val	Gly	Gly	Asp	Gly	Ala	Val	Pro	Leu	Met	Lys	Ala
		275					280					285			
Tyr	Thr	Ala	Gly	Glu	His	Arg	Leu	Ser	Ser	Ala	Tyr	Ser	Phe	Asp	Phe
	290					295					300				
Leu	Tyr	Ala	Pro	Ala	Leu	Thr	Gly	Glu	Leu	Val	Ala	Asn	Ala	Leu	Ala
305					310				315					320	
Gln	Trp	Thr	Gly	Lys	Pro	Gly	Ala	Asp	Gly	Leu	Ser	Glu	Gly	Trp	Pro
				325					330					335	
Ser	Trp	Ala	Phe	Glu	Asn	His	Asp	Ala	Pro	Arg	His	Ile	Ser	Arg	Trp
			340					345					350		
Val	Gly	Glu	Glu	His	Arg	Ala	Ala	Phe	Ala	Arg	Met	Ser	Leu	Val	Leu
		355				360						365			
Leu	Ala	Ser	Leu	Arg	Gly	Asn	Met	Phe	Met	Tyr	Gln	Gly	Gln	Glu	Leu
	370					375					380				
Ala	Leu	Glu	Gln	Asp	Glu	Ile	Pro	Phe	His	Leu	Leu	Lys	Asp	Pro	Glu
385				390					395					400	
Ala	Ile	Ala	Asn	Trp	Pro	Leu	Thr	Leu	Ser	Arg	Asp	Gly	Val	Arg	Thr
			405					410						415	
Pro	Met	Pro	Trp	Asp	Ser	Gln	Ala	Phe	His	Ala	Gly	Phe	Thr	Ser	Gly
			420					425					430		
Glu	Pro	Trp	Leu	Pro	Leu	Ser	Pro	Gly	Asn	Ile	Ala	Lys	Ala	Val	Asp
		435				440						445			
Val	Gln	Glu	Ala	Asp	Pro	Gln	Ser	Gln	Leu	His	Trp	Val	Arg	Arg	Val
	450					455					460				

P C L E u A l a L e u A r g A l a A l a A r g H i s L y s A l a L e u A r g L e u G l y A l a M e t G l u
 465 470 475 480
 H i s V a l H i s V a l G l n G l y A s p V a l L e u S e r P h e T h r A r g H i s A l a A r g
 485 490 495
 G l y G l u A r g V a l G l u C y s V a l P h e A s n L e u S e r A l a L y s T h r V a l A l a
 500 505 510
 H i s L y s A l a H i s L y s G l y G l u T h r L e u L e u T h r V a l A s n G l y A l a T h r
 515 520 525
 G l y A l a V a l L e u T h r P r o T y r G l y A l a L e u T r p T h r L y s L e u A l a
 530 535 540

<210> 17
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 17
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 gtctatctca tggatattaa taaggagcgg ctcgacctca taacagggtt cgccaagcga 180
 tacgctgccg agatgcatgc tgatctagag tttatcccta caatggatcg catagaggcg 240
 ataagggatg cagacttcgt cgtcaactca gccatgtacg gtggccacat gtactatgag 300
 cgtatgagag aaatatgtga gaggcacggc tattaccgag gaataaacag tgttgaatgg 360
 aacatgggtca gcgattacca caccatatgg ggttactacc agttcaaact agccatgagc 420
 attgccaaag atgtagagga atacgcgccc gacgcctggc ttatcaacgt cgccaaccct 480
 gtgttcgagc tgacaacact gatccagagg cacgtcaaga taaagatgat agggctctgc 540
 catggctacc atggcatcta taatgtgatc aaagaactcg ggctagacag ggatgagaca 600
 gagttcgagg tactcggtt caaccatgtg atctggctca caaagttcaa gtacagggga 660
 gaggaacgctt accccttact agataagtgg atcgaggaga aagcagagaa gtactgggag 720
 cattggagac aaacacaggt gaaccgcgtt gacattgact tgtctcctgc agcgatagac 780
 atgtacaaga gatacgggtc acttccggta ggagatactg tgcgtggagg cacgtggatg 840
 taccactggg atctcaagac gaagcagaaa tggatatggac cgacaggagg accagactcc 900
 gagataggct ggatgatgta tatagccttc ctaagcatgc agtcctcaaag attatacgaa 960
 gcactaatgg atcagaagca cccattagca gcacatatac cgccggagtg gagcgggtgaa 1020
 tccatagttc caataatcga tagcctcgcc aacaatagga ggggagaata cgttatcaac 1080
 acgttgaacc ttggtagtat accggggata ccggatagtg tagctgtcga gatgccagcc 1140
 cagatagatg gtaaaggagt gcaccgctac atattcgagc ccctcccca gaagataaga 1200
 gacctagtcc tactgcctag gatgaccggt atggagatgg cgttgacagc cttcctcgag 1260
 ggaggccgag aagtactcga ggactggcta cacatggatc cacgtaccaa gagcactgga 1320
 caggtacggg agacaatcga tgatctcctg aacatgcccg gtaacgagga gatgaagaag 1380
 catttcagct ag 1392

<210> 18
 <211> 463
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 18
 Met Glu Glu Glu Pro Arg Gly Lys Gly Leu Lys Ile Ala Phe Ile Gly
 1 5 10 15
 Ala Gly Ser Ala Val Trp Ser Ser Arg Ile Ile Ile Asp Leu Ile Leu
 20 25 30
 Ala Lys Ser Leu His Gly Ala Lys Val Tyr Leu Met Asp Ile Asn Lys
 35 40 45
 Glu Arg Leu Asp Leu Ile Thr Gly Phe Ala Lys Arg Tyr Ala Ala Glu
 50 55 60
 Met His Ala Asp Leu Glu Phe Ile Pro Thr Met Asp Arg Ile Glu Ala
 65 70 75 80

PC Ile Arg Asp Ala Asn Phe Val Val Asn Ser Ala Met Tyr Gly Gly His
 85 90 95
 Met Tyr Tyr Glu Arg Met Arg Glu Ile Cys Glu Arg His Gly Tyr Tyr
 100 105 110
 Arg Gly Ile Asn Ser Val Glu Trp Asn Met Val Ser Asp Tyr His Thr
 115 120 125
 Ile Trp Gly Tyr Tyr Gln Phe Lys Leu Ala Met Ser Ile Ala Lys Asp
 130 135 140
 Val Glu Glu Tyr Ala Pro Asp Ala Trp Leu Ile Asn Val Ala Asn Pro
 145 150 155 160
 Val Phe Glu Leu Thr Thr Leu Ile Gln Arg His Val Lys Ile Lys Met
 165 170 175
 Ile Gly Leu Cys His Gly Tyr His Gly Ile Tyr Asn Val Ile Lys Glu
 180 185 190
 Leu Gly Leu Asp Arg Asp Glu Thr Glu Phe Glu Val Leu Gly Phe Asn
 195 200 205
 His Val Ile Trp Leu Thr Lys Phe Lys Tyr Arg Gly Glu Asp Ala Tyr
 210 215 220
 Pro Leu Leu Asp Lys Trp Ile Glu Glu Lys Ala Glu Lys Tyr Trp Glu
 225 230 235 240
 His Trp Arg Gln Thr Gln Val Asn Pro Phe Asp Ile Asp Leu Ser Pro
 245 250 255
 Ala Ala Ile Asp Met Tyr Lys Arg Tyr Gly Leu Leu Pro Val Gly Asp
 260 265 270
 Thr Val Arg Gly Gly Thr Trp Met Tyr His Trp Asp Leu Lys Thr Lys
 275 280 285
 Gln Lys Trp Tyr Gly Pro Thr Gly Gly Pro Asp Ser Glu Ile Gly Trp
 290 295 300
 Met Met Tyr Ile Ala Phe Leu Ser Met Gln Leu Gln Arg Leu Tyr Glu
 305 310 315 320
 Ala Leu Met Asp Gln Lys His Pro Leu Ala Ala His Ile Pro Pro Glu
 325 330 335
 Trp Ser Gly Glu Ser Ile Val Pro Ile Ile Asp Ser Leu Ala Asn Asn
 340 345 350
 Arg Arg Gly Glu Tyr Val Ile Asn Thr Leu Asn Leu Gly Ser Ile Pro
 355 360 365
 Gly Ile Pro Asp Ser Val Ala Val Glu Met Pro Ala Gln Ile Asp Gly
 370 375 380
 Lys Gly Val His Arg Tyr Ile Phe Glu Pro Leu Pro Lys Lys Ile Arg
 385 390 395 400
 Asp Leu Val Leu Leu Pro Arg Met Thr Arg Met Glu Met Ala Leu Thr
 405 410 415
 Ala Phe Leu Glu Gly Gly Arg Glu Val Leu Glu Asp Trp Leu His Met
 420 425 430
 Asp Pro Arg Thr Lys Ser Thr Gly Gln Val Arg Glu Thr Ile Asp Asp
 435 440 445
 Leu Leu Asn Met Pro Gly Asn Glu Glu Met Lys Lys His Phe Ser
 450 455 460

<210> 19

<211> 1686

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 19

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aaaaagctcg	gggtagatgt	tctgtggcta	acgccaat	ataaatcacc	gcagcgggat	180
aatggatatg	atataagtga	ttattttgtt	attcaagaag	aatacggaac	aatggaggat	240
tttgatcttt	tagtaacaga	agcgcataag	cggggtctta	aagtcatcat	ggatattgtc	300
gttaatcata	catcaactga	acatgaatgg	tttcaagaag	ctaaaaaatc	gaaagataac	360

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PC TCGTACCGAGATTCTTATATCTGGGAAGGTCAAAAAGGAG atggaagtgc tccgacgaat 420
tggttttcaa aatttggggg atccgcgtgg gagcatgata acctcacaga acaatcgtat 480
ctgcatttgt ttgatgttac gcaagcggat ttgaactggg aaaacgagcg tgtgcgccgc 540
agcgtgtatg atatgatgac gtttttggtt gaaaaaggag tagatggatt tcgtctggac 600
gttattaatt taatttcaaa agatcagcgt ttttttagatg atgacgggtc cgttgcacca 660
ggagatggcc ggaaattcta caccgacggt cctcgcgtgc acgaatatat gcgggaaatg 720
aatcaagaag ttttttcaaa atatgatagt atgaccgttg gagaaatgtc gtccacaacc 780
gttgaccact gtattcagta ctctcatccg gaccgacgcg agcttagtat gacgtttaat 840
tttcatcatt tgaaagtcca ttaccggaat ggagaaaagt gggccctagc agattttgat 900
tttattaaat taaaagagat tctatcaact tggcaaacgg aaatgaataa aggtggggga 960
tggaatgcat tattttggtg caaccatgat cagcctcgcg ttgtttcacg ctatggagac 1020
gacgaactct atcataataa atctgctaaa atgctcgcga caacgattca tttgatgcag 1080
ggaacgcctt atatctatca aggcgaagaa ataggtatga caaacccgaa gttttcctct 1140
attgatgaat atagagatgt ggagtcattt aatgtgtatg aaataaaacg tgcacaagga 1200
atggacgaaa atgaaatttt ggaaatttta aaacataaat caagagataa ttcccgtaca 1260
ccggtgcaat ggaacgataa gccgaatgca ggttttcaaa aaggaaagcc atggattcat 1320
ccggccgata actaccgtaa aattaatgta gaaaaagcgt tagaggataa agattcaatc 1380
ttttattttt atcaaaagct tattgcactg cgcaagcagt acgagattat cacctatgga 1440
aactatgaat tgattcttgg agaagacgag cagattttcg cttatatccg aaatggagca 1500
gatgaaaagc tgctcgtgat aaacaatttc tacggcagcg agaaaatttt tgaactgcca 1560
gaaaatctaa cttttgaagg atatcatagt gaaatattgc tgtctaacta cgaagattca 1620
ccaaaggaat tcaagcgagt cttacttcgg ccgtatgaat caatcgtgta tcatttaaaa 1680
aaatag 1686

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<210> 20
 <211> 561
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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<400> 20
Met Gln Glu Pro Trp Trp Lys Lys Ser Val Val Tyr Gln Ile Tyr Pro
1          5          10          15
Lys Ser Phe Tyr Asp Thr Thr Gly Asn Gly Val Gly Asp Ile Ala Gly
20          25          30
Ile Ile Glu Lys Leu Asp Tyr Leu Lys Lys Leu Gly Val Asp Val Leu
35          40          45
Trp Leu Thr Pro Ile Tyr Lys Ser Pro Gln Arg Asp Asn Gly Tyr Asp
50          55          60
Ile Ser Asp Tyr Phe Val Ile Gln Glu Glu Tyr Gly Thr Met Glu Asp
65          70          75          80
Phe Asp Leu Leu Val Thr Glu Ala His Lys Arg Gly Leu Lys Val Ile
85          90          95

Met Asp Ile Val Val Asn His Thr Ser Thr Glu His Glu Trp Phe Gln
100          105          110
Glu Ala Lys Lys Ser Lys Asp Asn Pro Tyr Arg Asp Phe Tyr Ile Trp
115          120          125
Lys Asp Gln Lys Glu Asp Gly Ser Ala Pro Thr Asn Trp Val Ser Lys
130          135          140
Phe Gly Gly Ser Ala Trp Glu His Asp Asn Leu Thr Glu Gln Ser Tyr
145          150          155          160
Leu His Leu Phe Asp Val Thr Gln Ala Asp Leu Asn Trp Glu Asn Glu
165          170          175
Arg Val Arg Arg Ser Val Tyr Asp Met Met Thr Phe Trp Phe Glu Lys
180          185          190
Gly Val Asp Gly Phe Arg Leu Asp Val Ile Asn Leu Ile Ser Lys Asp
195          200          205
Gln Arg Phe Leu Asp Asp Asp Gly Ser Val Ala Pro Gly Asp Gly Arg
210          215          220
Lys Phe Tyr Thr Asp Gly Pro Arg Val His Glu Tyr Met Arg Glu Met
225          230          235          240

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P C Asn Glu Glu Val Phe Ser Lys Tyr Asp Ser Met Thr Val Gly Glu Met
 245 250 255
 Ser Ser Thr Thr Val Asp His Cys Ile Gln Tyr Ser His Pro Asp Arg
 260 265 270
 Arg Glu Leu Ser Met Thr Phe Asn Phe His His Leu Lys Val Asp Tyr
 275 280 285
 Pro Asn Gly Glu Lys Trp Ala Leu Ala Asp Phe Asp Phe Ile Lys Leu
 290 295 300
 Lys Glu Ile Leu Ser Thr Trp Gln Thr Glu Met Asn Lys Gly Gly Gly
 305 310 315 320
 Trp Asn Ala Leu Phe Trp Cys Asn His Asp Gln Pro Arg Val Val Ser
 325 330 335
 Arg Tyr Gly Asp Asp Glu Leu Tyr His Asn Lys Ser Ala Lys Met Leu
 340 345 350
 Ala Thr Thr Ile His Leu Met Gln Gly Thr Pro Tyr Ile Tyr Gln Gly
 355 360 365
 Glu Glu Ile Gly Met Thr Asn Pro Lys Phe Ser Ser Ile Asp Glu Tyr
 370 375 380
 Arg Asp Val Glu Ser Leu Asn Val Tyr Glu Ile Lys Arg Ala Gln Gly
 385 390 395 400
 Met Asp Glu Asn Glu Ile Leu Glu Ile Leu Lys His Lys Ser Arg Asp
 405 410 415
 Asn Ser Arg Thr Pro Val Gln Trp Asn Asp Lys Pro Asn Ala Gly Phe
 420 425 430
 Thr Lys Gly Lys Pro Trp Ile His Pro Ala Asp Asn Tyr Arg Lys Ile
 435 440 445
 Asn Val Glu Lys Ala Leu Glu Asp Lys Asp Ser Ile Phe Tyr Phe Tyr
 450 455 460
 Gln Lys Leu Ile Ala Leu Arg Lys Gln Tyr Glu Ile Ile Thr Tyr Gly
 465 470 475 480
 Asn Tyr Glu Leu Ile Leu Gly Glu Asp Glu Gln Ile Phe Ala Tyr Ile
 485 490 495
 Arg Asn Gly Ala Asp Glu Lys Leu Leu Val Ile Asn Asn Phe Tyr Gly
 500 505 510
 Ser Glu Lys Ile Phe Glu Leu Pro Glu Asn Leu Thr Phe Glu Gly Tyr
 515 520 525
 His Ser Glu Ile Leu Leu Ser Asn Tyr Glu Asp Ser Pro Lys Glu Phe
 530 535 540
 Lys Arg Val Leu Leu Arg Pro Tyr Glu Ser Ile Val Tyr His Leu Lys
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 Lys

<210> 21
 <211> 1443
 <212> DNA
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<400> 21
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 gacgaagaaa ggctagatgc ggttctgacc atagcaaaaa agtacgttga agaagtggga 180
 gccgacctga agtttgaaaa gacaacaagc gtagacgaag ccacgcgtga tgcggatttt 240
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 gtgaaccacg gaatatgggt gaacagggtc agatacaacg gcgaggatgc gtaccactt 660
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<210> 22
 <211> 480
 <212> PRT
 <213> Eukaryote

<400> 22

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Ser	Thr	Val	Thr	Leu	Met	Asp	Ile	Asp	Glu	Glu	Arg	Leu	Asp	Ala	Val
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		50				55					60				
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Val	Ile	Asn	Thr	Ala	Met	Val	Gly	Gly	His	Thr	Tyr	Leu	Glu	Lys	Val
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Arg	Arg	Ile	Ser	Glu	Lys	Tyr	Gly	Tyr	Tyr	Arg	Gly	Ile	Asp	Ala	Gln
			100					105					110		
Glu	Phe	Asn	Met	Val	Ser	Asp	Tyr	Tyr	Thr	Phe	Ser	Asn	Tyr	Asn	Gln
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Lys	Ala	Trp	Tyr	Leu	Gln	Ala	Ala	Asn	Pro	Val	Phe	Glu	Gly	Thr	Thr
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			165						170					175	
His	Tyr	Gly	Val	Met	Glu	Ile	Val	Glu	Lys	Leu	Gly	Leu	Glu	Glu	Asn
			180					185					190		
Arg	Val	Asp	Trp	Gln	Val	Ala	Gly	Val	Asn	His	Gly	Ile	Trp	Leu	Asn
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		210			215						220				
Ile	Ser	Glu	Lys	Ser	Lys	Asp	Trp	Lys	Pro	Glu	Asn	Pro	Phe	Asn	Asp
225					230				235						240
Gln	Leu	Ser	Pro	Ala	Ala	Ile	Asp	Met	Tyr	Arg	Phe	Tyr	Gly	Val	Met
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Pro	Ile	Gly	Asp	Thr	Val	Arg	Asn	Ser	Ser	Trp	Arg	Tyr	His	Arg	Asp
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Leu	Glu	Thr	Lys	Lys	Lys	Trp	Tyr	Gly	Glu	Pro	Trp	Gly	Gly	Ala	Asp
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Ser	Glu	Ile	Gly	Trp	Lys	Trp	Tyr	Gln	Asp	Thr	Leu	Gly	Lys	Val	Thr
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Glu	Ile	Thr	Lys	Lys	Val	Ala	Lys	Phe	Ile	Lys	Glu	Asn	Pro	Ser	Ala
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Arg	Leu	Ser	Asp	Leu	Gly	Ser	Val	Leu	Gly	Lys	Asp	Leu	Ser	Glu	Lys
				325					330					335	
Gln	Phe	Val	Leu	Glu	Val	Glu	Lys	Ile	Leu	Asp	Pro	Glu	Lys	Lys	Ser
			340				345						350		
Gly	Glu	Gln	His	Ile	Pro	Phe	Ile	Asp	Ala	Leu	Leu	Asn	Asp	Asn	Arg
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PC Ser Arg Phe Val Ile Asn Ile Pro Asn Lys Gly Ile Ile Gln Gly Ile
 370 375 380
 Asp Asp Asp Val Val Val Glu Val Pro Ala Val Val Asp Arg Asp Gly
 385 390 395 400
 Ile His Pro Glu Lys Ile Ala Pro Pro Leu Pro Glu Arg Val Val Lys
 405 410 415
 Tyr Tyr Leu Arg Pro Arg Ile Met Arg Met Glu Met Ala Leu Glu Ala
 420 425 430
 Phe Leu Thr Gly Asp Ile Arg Ile Ile Lys Glu Val Leu Tyr Arg Asp
 435 440 445
 Pro Arg Thr Lys Ser Asp Glu Gln Val Glu Lys Val Ile Glu Glu Ile
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 Leu Ser Leu Pro Glu Asn Glu Glu Met Arg Lys Asn Tyr Leu Lys Lys
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 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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 aaaaagctcg gggtagatgt tctgtggcta acgccaattt ataaatcacc gcagcgggat 180
 aatggatatg atataagtga ttattttgtt attcaagaag aatacgggaac aatggaggat 240
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 ccgtaccgag atttttatat ttggaaagat caaaaagaag atggaagtgc tccgacgaat 420
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<210> 24
 <211> 561
 <212> PRT
 <213> Unknown

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<400> 24

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 35 40 45
 Trp Leu Thr Pro Ile Tyr Lys Ser Pro Gln Arg Asp Asn Gly Tyr Asp
 50 55 60
 Ile Ser Asp Tyr Phe Val Ile Gln Glu Glu Tyr Gly Thr Met Glu Asp
 65 70 75 80
 Phe Asp Leu Leu Val Thr Glu Ala His Lys Arg Gly Leu Lys Val Ile
 85 90 95
 Met Asp Ile Val Val Asn His Thr Ser Thr Glu His Glu Trp Phe Gln
 100 105 110
 Glu Ala Lys Lys Ser Lys Asp Asn Pro Tyr Arg Asp Phe Tyr Ile Trp
 115 120 125
 Lys Asp Gln Lys Glu Asp Gly Ser Ala Pro Thr Asn Trp Val Ser Lys
 130 135 140
 Phe Gly Gly Ser Ala Trp Glu His Asp Asn Leu Thr Glu Gln Ser Tyr
 145 150 155 160
 Leu His Leu Phe Asp Val Thr Gln Ala Asp Leu Asn Trp Glu Asn Glu
 165 170 175
 Arg Val Arg Arg Ser Val Tyr Asp Met Met Thr Phe Trp Phe Glu Lys
 180 185 190
 Gly Val Asp Gly Phe Arg Leu Asp Val Ile Asn Leu Ile Ser Lys Asp
 195 200 205
 Gln Arg Phe Leu Asp Asp Asp Gly Ser Val Ala Pro Gly Asp Gly Arg
 210 215 220
 Lys Phe Tyr Thr Asp Gly Pro Arg Val His Glu Tyr Met Arg Glu Met
 225 230 235 240
 Asn Gln Glu Val Phe Ser Lys Tyr Asp Ser Met Thr Val Gly Glu Met
 245 250 255
 Ser Ser Thr Thr Val Asp His Cys Ile Gln Tyr Ser His Pro Asp Arg
 260 265 270
 Arg Glu Leu Ser Met Thr Phe Asn Phe His His Leu Lys Val Asp Tyr
 275 280 285
 Pro Asn Gly Glu Lys Trp Ala Leu Ala Asp Phe Asp Phe Ile Lys Leu
 290 295 300
 Lys Glu Ile Leu Ser Thr Trp Gln Thr Glu Met Asn Lys Gly Gly Gly
 305 310 315 320
 Trp Asn Ala Leu Phe Trp Cys Asn His Asp Gln Pro Arg Val Val Ser
 325 330 335
 Arg Tyr Gly Asp Asp Glu Leu Tyr His Asn Lys Ser Ala Lys Met Leu
 340 345 350
 Ala Thr Thr Ile His Leu Met Gln Gly Thr Pro Tyr Ile Tyr Gln Gly
 355 360 365
 Glu Glu Ile Gly Met Thr Asn Pro Lys Phe Ser Ser Ile Asp Glu Tyr
 370 375 380
 Arg Asp Val Glu Ser Leu Asn Val Tyr Glu Ile Lys Arg Ala Gln Gly
 385 390 395 400
 Met Asp Glu Asn Glu Ile Leu Glu Ile Leu Lys His Lys Ser Arg Asp
 405 410 415
 Asn Ser Arg Thr Pro Val Gln Trp Asn Asp Lys Pro Asn Ala Gly Phe
 420 425 430
 Thr Lys Gly Lys Pro Trp Ile His Pro Ala Asp Asn Tyr Arg Lys Ile
 435 440 445
 Asn Val Glu Lys Ala Leu Glu Asp Lys Asp Ser Ile Phe Tyr Phe Tyr
 450 455 460
 Gln Lys Leu Ile Ala Leu Arg Lys Gln Tyr Glu Ile Ile Thr Tyr Gly
 465 470 475 480
 Asn Tyr Glu Leu Ile Leu Gly Glu Asp Glu Gln Ile Phe Ala Tyr Ile
 485 490 495
 Arg Asn Gly Ala Asp Glu Lys Leu Leu Val Ile Asn Asn Phe Tyr Gly
 500 505 510

P	C	Ser	Glu	Thr	Ala	Phe	Glu	Leu	Pro	Glu	Asp	Leu	Thr	Phe	Glu	Gly	Tyr
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His	Ser	Glu	Ile	Leu	Leu	Ser	Asn	Tyr	Glu	Asp	Ser	Pro	Lys	Glu	Phe		
		530				535					540						
Lys	Arg	Val	Leu	Leu	Arg	Pro	Tyr	Glu	Ser	Ile	Val	Tyr	His	Leu	Lys		
545					550					555					560		
Lys																	